

```

Emhtg7:Al158158      Begin: 199213  End: 199231
! Al158158 Human DNA sequence *** SEQ...  77  299  77  284.0  1.7e-09

Emhtg2:Ac011126      Begin: 102317  End: 102347  Strand: -
! Ac011126 Homo sapiens chromosome 18...  88  299  94  285.4  1.9e-09
Emhtg6:Ac023834      Begin: 88592   End: 88631
! Ac023834 Mus musculus clone RP23-36...  77  298  128  283.2  2e-09
Emhtg2:Ac012454      Begin: 31435   End: 31452  Strand: -
! Ac012454 Homo sapiens clone RP11-43...  75  298  81  283.6  2.1e-09
Emhtg1:Ac008076      Begin: 81374   End: 81390  Strand: -
! Ac008076 Homo sapiens chromosome 4,...  75  297  76  282.0  2.3e-09
Emhtg6:Al135910      Begin: 7400    End: 7415  Strand: -
! Al135910 Human DNA sequence *** SEQ...  71  297  71  282.8  2.4e-09

Emhtg1:Ac009259      Begin: 71143   End: 71187  Strand: -
! Ac009259 Trypanosoma brucei chromos...  81  297  96  283.1  2.5e-09
Emhtg2:Ac010729      Begin: 9984    End: 10012  Strand: -
! Ac010729 Homo sapiens clone RP11-35...  72  296  73  281.2  2.7e-09
Emhtg6:Ac024163      Begin: 134290  End: 134322
! Ac024163 Homo sapiens chromosome 3p...  84  296  84  281.9  2.8e-09
Emhtg2:Ac010413      Begin: 177374  End: 177391  Strand: -
! Ac010413 Homo sapiens chromosome 5 ...  81  294  81  277.9  3.2e-09
Emhtg2:Ac011723      Begin: 53668   End: 53684
! Ac011723 Homo sapiens chromosome 18...  76  295  76  281.3  3.3e-09

Emhtg1:Ac008367      Begin: 117968  End: 117995
! Ac008367 Drosophila melanogaster ch...  75  294  86  278.7  3.4e-09
\\End of List

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9904247_3.Dna
Emfun:Sc9718

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ID  SC9718      standard; DNA; FUN; 35811 BP.
AC  Z49702; Z71257;
SV  Z49702.1
DT  21-MAY-1995 (Rel. 43, Created)
DT  11-AUG-1997 (Rel. 52, Last updated, Version 1)
DE  S.cerevisiae chromosome XIII cosmid 9718.
KW  acetolactate synthase; aldehyde dehydrogenase; beta-transducin;
KW  Coiled coil protein; folylpolyglutamate synthase; GAL5; glycosyl hydrolase;

KW  guanine nucleotide binding protein; ILV2; membrane protein;
KW  myosin homologue; PGM2; phosphoglucomutase; protein kinase; SMR1;

KW  succinate dehydrogenase; transfer RNA-Leu; transfer RNA-Lys; YKR2; YPK2.
OS  Saccharomyces cerevisiae (baker's yeast)
OC  Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC  Saccharomycetaceae; Saccharomyces.
RN  [1]
RP  1-35811
RA  Hunt S., Bowman S.;
RT  ;
RL  Unpublished.
RN  [2]
RP  1-35811
RA  Barrell B., Rajandream M.A.;
RT  ;
RL  Submitted (19-MAY-1995) to the EMBL/GenBank/DDBJ databases.
RL  Saccharomyces cerevisiae chromosome XIII sequencing project, Sanger Centre,

RL  Hinxton Hall, Hinxton, Cambridge CB10 1RQ E-mail: barrell@sanger.ac.uk
DR  SGD; S0004709; YMR103C.
DR  SGD; S0004710; YPK2.

DR  SGD; S0004711; PGM2.
DR  SGD; S0004712; YKU80.
DR  SGD; S0004713; YMR107W.
DR  SGD; S0004714; ILV2.
DR  SGD; S0004715; MYO5.

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DR SGD; S0004716; YMR110C.
DR SGD; S0004717; YMR111C.
DR SGD; S0004718; MED11.
DR SGD; S0004719; YMR113W.
DR SGD; S0004720; YMR114C.
DR SGD; S0004721; YMR115W.
DR SGD; S0004722; ASC1.
DR SGD; S0004723; SPC24.
DR SGD; S0004724; YMR118C.
DR SWISS-PROT; P07342; ILVB_YEAST.
DR SWISS-PROT; P18961; YPK2_YEAST.
DR SWISS-PROT; P37012; PGM2_YEAST.
DR SWISS-PROT; P38011; GBLP_YEAST.
DR SWISS-PROT; P54074; YM08_YEAST.
DR SWISS-PROT; Q03177; YMZ2_YEAST.
DR SWISS-PROT; Q04436; YMZ3_YEAST.

DR SWISS-PROT; Q04437; HDF2_YEAST. . . .

SCORES Init1: 2470 Initn: 2470 Opt: 2476 z-score: 2560.5 E(): 0
99.8% identity in 497 bp overlap

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          10      20      30
9904247_3.Dn GCAGAAATGATGAAGGGTGTAGCGCCGTC
Sc9718      AAAAGTCATCTGGCACGTTTAATTATCAGAGCAGAAATGATGAAGGGTGTAGCGCCGTC
          11680      11690      11700      11710      11720      11730

          40      50      60      70      80      90
9904247_3.Dn CACTGATGTGCCTGGTAGTCATGATTTACGTATAACTAACACATCATGAGGACGGCGGCG
Sc9718      CACTGATGTGCCTGGTAGTCATGATTTACGTATAACTAACACATCATGAGGACGGCGGCG
          11740      11750      11760      11770      11780      11790

          100      110      120      130      140      150
9904247_3.Dn TCACCCCAACGCAAAAGAGTGACTTCCCTGCGCTTTGCCAAAACCCCATACATCGCCATC
Sc9718      TCACCCCAACGCAAAAGAGTGACTTCCCTGCGCTTTGCCAAAACCCCATACATCGCCATC
          11800      11810      11820      11830      11840      11850

          160      170      180      190      200      210
9904247_3.Dn TGGCTCCTGGCAGGGCGGTTGATGGACATCAGCCGCCTCCCTTAATTGCTAAAGCCTCCA
Sc9718      TGGCTCCTGGCAGGGCGGTTGATGGACATCAGCCGCCTCCCTTAATTGCTAAAGCCTCCA
          11860      11870      11880      11890      11900      11910

          220      230      240      250      260      270
9904247_3.Dn CAAGGCACAATTAAGCAATATTTCTGGGAAAGTACACCAAGTCAGTTTGCGCTTTTATGACT
Sc9718      CAAGGCACAATTAAGCAATATTTCTGGGAAAGTACACCAAGTCAGTTTGCGCTTTTATGACT
          11920      11930      11940      11950      11960      11970

          280      290      300      310      320      330
9904247_3.Dn GGGTTCTAAGGTACTAGATGTGAAGTAGTGGTGACAGAATCAGGGAGATAAGAGGGAGCA
Sc9718      GGGTTCTAAGGTACTAGATGTGAAGTAGTGGTGACAGAATCAGGGAGATAAGAGGGAGCA
          11980      11990      12000      12010      12020      12030

          340      350      360      370      380      390
9904247_3.Dn GGGTGGGGTAATGATGTGCGATAACAATCTTGCTTGGCTAATCACCCCCATATCTTGTAG
Sc9718      GGGTGGGGTAATGATGTGCGATAACAATCTTGCTTGGCTAATCACCCCCATATCTTGTAG
          12040      12050      12060      12070      12080      12090
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          400      410      420      430      440      450
9904247_3.Dn TGAGTATATAAATAGGAGCCTCCCTTCTATTGCAACTCCATAAAATTTTTTTTGTAGC
Sc9718      TGAGTATATAAATAGGAGCCTCCCTTCTATTGCAACTCCATAAAATTTTTTTTGTAGC
          12100    12110    12120    12130    12140    12150

          460      470      480      490
9904247_3.Dn CACTTCTGTAACAAGATAAAATAAAACCAACTAATCGAGATATCACAT
          ||||||||||||||||||||||||||||||||||||||||
Sc9718      CACTTCTGTAACAAGATAAAATAAAACCAACTAATCGAGATATCAAATATGGGTTAGTTTTT
          12160    12170    12180    12190    12200    12210

Sc9718      GGGACGCATTTCGCAGTATACGACAAGAAAAAGCACGCAGATCCAAGTGTATATGGAGGAA
          12220    12230    12240    12250    12260    12270

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9904247_3.Dna /rev
Emhtg6:Ac023173

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ID  AC023173   standard; DNA; HTG; 191479 BP.
AC  AC023173;
SV  AC023173.1
DT  14-FEB-2000 (Rel. 62, Created)
DT  14-FEB-2000 (Rel. 62, Last updated, Version 1)
DE  Mus musculus chromosome 6 clone RP23-11G22 strain C57BL6/J, WORKING
DE  DRAFT SEQUENCE, 11 unordered pieces.
KW  HTG; HTGS_DRAFT; HTGS_PHASE1.

OS  Mus musculus (house mouse)
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Teleostomi;
OC  Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

OC  Mus.
RN  [1]
RP  1-191479
RA  Beckstrom-Sternberg S.M., Benjamin B., Bouffard G.G., Dietrich N.L.,
RA  Eagle W.O., Gan W., Gupta J., Ho S.-L., Huang M.C., Idol J., Jamison D.C.,
RA  Lee-Lin S.-Q., Maduro Q.L., Maduro V.B., Mastrian S.D., McCloskey J.C.,
RA  Morse E., Ojodu M.A., Pearson R., Stantripop S., Summers T.J., Thomas J.W.,

RA  Thomas P.J., Tiongson E.E., Touchman J.W., Tran J.T., Vogt J.L.,
RA  Walker M.A., Wetherby K.D., Green E.D.;

RT  "NISC Mouse Sequencing Initiative";
RL  Unpublished.
RN  [2]
RP  1-191479
RA  Green E.D.;
RT  ;
RL  Submitted (09-FEB-2000) to the EMBL/GenBank/DBJ databases.
RL  NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD
RL  20877, USA
CC  -- Genome Center
CC  Center: NIH Intramural Sequencing Center
CC  Center code: NISC
CC  Web site: http://www.nisc.nih.gov
CC  Contact: nisc_mouse@nhgri.nih.gov
CC  -- Project Information
CC  Center project name: ya
CC  Center clone name: 011G22
CC  -- Summary Statistics
CC  Sequencing vector: plasmid; n/a; 100% of reads

CC  Chemistry: Dye-terminator Big Dye; 100% of reads
CC  Assembly program: Phrap; version 0.990319
CC  Consensus quality: 184222 bases at least Q40
CC  Consensus quality: 187020 bases at least Q30
CC  Consensus quality: 188777 bases at least Q20
CC  Insert size: 180000; pulse-field-gel

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